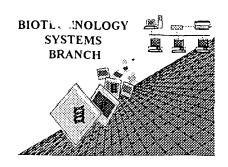


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

| Application Serial Number: | 09/100,696 |
|----------------------------|------------|
| Source: | PCT09 |
| Date Processed by STIC: | 1/23/2001 |

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUM

| ΔΤΤ | N. NEW BIH ES CASES. | PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | |
|-----|-------------------------|--|----|
| 1 | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line. | |
| ' | _ vviapped ivadicies | This may occur if your file was retrieved in a word processor after creating it. | |
| | | Please adjust your right margin to .3, as this will prevent "wrapping". | |
| | _ Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line. | |
| | | This may occur if your file was retrieved in a word processor after creating it. | |
| | | Please adjust your right margin to .3, as this will prevent "wrapping". | |
| 3 | Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. | |
| | | | |
| 4 | Misaligned Amino Acid | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs | |
| - | Numbering | between the numbering. It is recommended to delete any tabs and use spacing between the numbers. | |
| 5 | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. | |
| | _ | Please ensure your subsequent submission is saved in ASCII text so that it can be processed. | |
| 6 | Variable Length | Sequence(s) contain n's or Xaa's which represented more than one residue. | |
| - | | As per the rules, each n or Xaa can only represent a single residue. | |
| | | Please present the maximum number of each residue having variable length and | |
| | | indicate in the (ix) feature section that some may be missing. | |
| | | | |
| 7 | Patentin ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid | |
| · | | sequence(s) . Normally, PatentIn would automatically generate this section from the | |
| | | previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section | |
| | | to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> | |
| | | sections for Artificial or Unknown sequences. | |
| | 01: 10 | Control of the state of the state of the following format for each attinged accuracy. | |
| 8 | _ Skipped Sequences | Sequence(s) missing. If intentional, please use the following format for each skipped sequence: | |
| | (OLD RULES) | (2) INFORMATION FOR SEQ ID NO:X: | |
| | | (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") | |
| | | (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: | |
| | | This sequence is intentionally skipped | |
| | | Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). | |
| 9 | Skipped Sequences | Sequence(s) missing. If intentional, please use the following format for each skipped sequence. | |
| · - | (NEW RULES) | <210> sequence id number | |
| | (| \$400> sequence id number | |
| | | 000 | |
| 0 | Use of n's or Xaa's | Use of n's and/or Xaa's have been detected in the Sequence Listing. | |
| · | (NEW RULES) | Use of <220> to <223> is MANDATORY if n's or Xaa's are present. | |
| | (MENN MOLES) | In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaairepresents. | |
| | | */ | |
| 1 | Use of <213>Organism | Sequence(s) are missing this mandatory field or its response. | |
| | (NEW RULES) | | |
| 2 | Use of <220>Feature | Sequence(s) are missing the <220>Feature and associated headings. | |
| | (NEW RULES) | Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown" | |
| | 5/ | Please explain source of genetic material in <220> to <223> section. | |
| | | (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rule | s) |
| _ | | | |
| 3 | Patentin ver. 2.0 "bug" | Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted | |

Instead, please use "File Manager" or any other means to copy file to floppy disk.

"file, Tesalting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

PCT09

RAW SEQUENCE LISTING DATE: 01/23/2001
PATENT APPLICATION: US/09/700,696 TIME: 11:11:40

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01232001\1700696.raw

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      5 <120> TITLE OF INVENTION: A novel polypeptide hormone phosphatonin
      7 <130> FILE REFERENCE: D1583PCT
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/700,696
C--> 10 <141> CURRENT FILING DATE: 2000-11-17
    12 <160> NUMBER OF SEQ ID NOS: 25
    14 <170> SOFTWARE: Patentin Ver. 2.1
    16 <210> SEQ ID NO: 1
    17 <211> LENGTH: 1655
    18 <212> TYPE: DNA
    19 <213> ORGANISM: Homo sapiens
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    22 <221> NAME/KEY: CDS
    23 <222> LOCATION: (1)..(1290)
    25 <400> SEQUENCE: 1
    26 gtg aat aaa gaa tat agt atc agt aac aaa gag aat act cac aat ggc
    27 Val Asn Lys Glu Tyr Ser Ile Ser Asn Lys Glu Asn Thr His Asn Gly
    28 1 .
                                          10
    30 ctg agg atg tca att tat cct aag tca act ggg aat aaa ggg ttt gag
                                                                         96
    31 Leu Arg Met Ser Ile Tyr Pro Lys Ser Thr Gly Asn Lys Gly Phe Glu
    32
                 20
                                      25
    34 gat gga gat gat get ate age aaa eta eat gae caa gaa gaa tat gge
                                                                         144
    35 Asp Gly Asp Asp Ala Ile Ser Lys Leu His Asp Gln Glu Glu Tyr Gly
    36
              35
                                   40
                                                       45
    38 gca gct ctc atc aga aat aac atg caa cat ata atg ggg cca gtg act
                                                                         192
    39 Ala Ala Leu Ile Arg Asn Asn Met Gln His Ile Met Gly Pro Val Thr
    40 50
                              55
                                                   60
    42 gcg att aaa ctc ctg ggg gaa gaa aac aaa gag aac aca cct agg aat
                                                                         240
    43 Ala Tle Lys Leu Leu Gly Glu Glu Asn Lys Glu Asn Thr Pro Arg Asn
                                               75
    46 gtt eta aac ata ate eea gea agt atg aat tat get aaa gea eac teg
                                                                         288
    47 Val Leu Asn Ile Ile Pro Ala Ser Met Asn Tyr Ala Lys Ala His Ser
                       85
                                          90
    50 aag gat aaa aag aag oot caa aga gat too caa goo cag aaa agt coa
    51 Lys Asp Lys Lys Lys Pro Gln Arg Asp Ser Gln Ala Cln Lys Ser Pro
                 100
                                      105
    54 gta aaa agc aaa agc acc cat cgt att caa cac aac att gac tac cta
                                                                         384
    55 Val Lys Ser Lys Ser Thr His Arg Ile Gln His Asn Ile Asp Tyr Leu
                                 1.20
                                                     125
    58 aaa cat etc tea aaa gte aaa aaa ate eec agt gat ttt gaa gge age
                                                                         432
    59 Lys His Leu Ser Lys Val Lys Lys Ile Pro Ser Asp Phe Glu Gly Ser
    60 1.30
                             1.35
                                                  140
    62 ggt tat aca gat ctt caa gag aga ggg gac aat gat ata tot cot tto
                                                                        480
    63 Gly Tyr Thr Asp Leu Gln Glu Arg Gly Asp Asn Asp Ile Ser Pro Phe
                          150
                                              155
    66 agt ggg gac ggc caa cot tit aag gac att cot ggt aaa gga gaa got
                                                                         528
    67 Ser Gly Asp Gly Gln Pro Phe Lys Asp Ile Pro Gly Lys Gly Glu Ala
```

Does Not Comply
Corrected Diskette Needed

m45

 RAW SEQUENCE LISTING
 DATE: 01/23/2001

 PATENT APPLICATION: US/09/700,696
 TIME: 11:11:40

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01232001\I700696.raw

| co | | | | | 1.65 | | | | | 170 | | | | | | | |
|------|------|-----|------|-------------------|-------|--------|-------|-------|----------|-------|--------|-------|-------|-----|-------|-------|--------|
| 68 | | | | | 165 | ~ | | | ~ 5. 4. | 170 | | | ~~~ | | 175 | | c7. |
| | | | | gac | | | | | | | | | | | | | 576 |
| | unr | GIY | Pro | Asp | ren | G 1.11 | GTÄ | ьys | • | 11.6 | GJI | Thr | GLY | | A.J.a | GIA | |
| 72 | | | | 1.80 | | 4. | | | 1.85 | | | | | 190 | | t | COL |
| | | | | get | - | • | | | | - | | | _ | | - " | | 624 |
| | Pro | ser | | Ala | GIU | ser | Thr | | Leu | Asp | Thr | Lys | - | Pro | GTA | Tyr | |
| 76 | | | 195 | | | | | 200 | | | | ٠ | 205 | | | | 670 |
| | | | | cca | | | | | | | | | | | | | 672 |
| | Asn | | TIe | Pro | Glu | Arg | | G.L.u | Asn | GTÄ | Gly | | Thr | 11e | GLY | Thr | |
| 80 | | 210 | | | | | 215 | | | | | 220 | | | | | 200 |
| | | | | act | | | | | | | | | | | | | 720 |
| | _ | Asp | G.Lu | Thr | Ala | _ | GLu | Ala | Asp | A.La | | Asp | Val | ser | Leu | | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| | | | | aac | | | | | | | | | | | | | 768 |
| | GLu | GLy | Ser | Asn | | He | Met. | Gly | ser | | Asn | Phe | Lys | GIu | | Pro | |
| 88 | | | | | 245 | | | | | 250 | | | | | 255 | | |
| | | - | | gga | | - | | | - | | - | | | - | | | 816 |
| | GTA | Arg | GLu | Gly | Asn | Arg | Val | Asp | | GLY | ser | Gln | Asn | | His | GIn | |
| 92 | | | | 260 | | | | | 265 | | | | | 270 | | | |
| | | | | gag | | | | | | • | | | | - | | - | 864 |
| | GT.A | Lys | | Glu | Phe | Hi.s | Туr | | Pro | A.l.a | Pro | Ser | - | Glu | Lys | Arg | |
| 96 | | | 275 | | | | | 280 | | | | | 285 | | | | |
| | | - | - | agt. | | | ** | - | | | | | | | - | | 912 |
| | • | | | ser | ser | Asp | | | GLu | ser | Thr | | _ | Asn | GIu | He | |
| 100 | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | | | | | | | _ | | _ | | | - | - | | | t aat | 960 |
| | | - | Asr | ı Gly | Lys | - | | Thr | : Arg | Liys | • | | . Asp | His | se | r Asn | |
| | 305 | | | | | 31.0 | | | | | 31.5 | | | | | 320 | |
| | | | | | | | | - | | | | | | _ | | a aac | 1008 |
| | _ | Asn | GII | A.La | | | Asn | Glu | LLYS | | - | Phe | Pro | Ser | _ | s Gly | |
| 108 | | | | | 325 | | | | | 330 | | | | | 33 | | 1056 |
| | | | | | | | | | | | | | | | | aatc | 1.056 |
| | _ | ser | GII | | | Pro |) ITE | Pro | | _ | G 1.5 | Leu | ASP | | | ı Ile | |
| 11.2 | | | | 340 | | | | | 345 | | | | | 350 | | | |
| | | | | - | | | | | | | - | | | | | a ata | 1,104 |
| | • | Asn | | | . Asp | Ser. | Pue | | | Pro | ser | 1 115 | | | 1.1.0 | e Ile | |
| 116 | | | 355 | | | | | 360 | | | | | 365 | | | | 3.1.50 |
| | | | | • | | | | | | | | _ | | | | t tot | 1152 |
| | | | _ | ' Arg | Lys | туг | | _ | . var | Pro | H J. S | _ | | ASn | ASI | n Ser | |
| 120 | | 370 | | | | | 375 | | | | | 380 | | | | | 1000 |
| | | | | • | | | | | 2. 0. 2. | | | | | | - | caa | 1200 |
| | | - | ASI | rräs | GTA | | | GIR | GJ.7 | răs | - | | Trp | GTA | Arg | g Gln | |
| | 385 | | | | | 390 | | | | | 395 | | | | | 400 | 7010 |
| | | | | | | | | | | | • | | _ | - | _ | agt. | 1.248 |
| | Pro | Hls | ser | Asn | | | Pue | ser | ser | | - | A.rg | Asp | Asp | | ser. | |
| 128 | | | | | 405 | | | | | 410 | | | | | 415 |) | |
| | | | | | • | | | | | | | | | | | | |
| | | | | . gac | - | | - | | | | - | | | | | | 1290 |
| | | | | gac Asp 420 | ser | | - | | | Glu | - | | | | 1 | | 1290 |

 RAW SEQUENCE LISTING
 DATE: 01/23/2001

 PATENT APPLICATION: US/09/700,696
 TIME: 11:11:40

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01232001\1700696.raw

134 tagtocacca ggagttocca goggggtgac agtotgaaga cotoqtoacc tgtgagttga 1350 136 tgtagaggag agccacctga cagctgacca ggtgaagaga ggatagagtg aagaactgag 1410 138 tgaqccaaga ateetggtet eettggggga attittgeta tettaatagt cacagtataa 1470 140 aattotatta aaggotataa tyttittaag caaaaaaaaa toattacaga totatgaaat 1530 142 aggtaacatt tgagtaggtg teatttaaaa atagttggtg aatgteacaa atgeetteta 1590 144 tyttytttyc tetytagaca tyaaaataaa caatatetet eyatyataaa aaaaaaaaa 1650 146 aaaaa 149 <210> SEQ 1D NO: 2 150 <211> LENGTH: 430 151 <212> TYPE: PRT 152 <213> ORGANISM: Homo sapiens 154 <400> SEQUENCE: 2 155 Val Asn Lys Glu Tyr Ser Ile Ser Asn Lys Glu Asn Thr His Asn Gly 1.56 1. 10 158 Leu Arg Met Ser Ile Tyr Pro Lys Ser Thr Gly Asn Lys Gly Phe Glu 159 20 25 30161 Asp Gly Asp Asp Ala Ile Ser Lys Leu His Asp Gln Glu Glu Tyr Gly 162 $$ 35 $$ 40 $$ 45 164 Ala Ala Leu Ile Arg Asn Asn Met Gln His Ile Met Gly Pro Val Thr $165 \qquad 50 \qquad 55 \qquad 60$ 167 Ala 11e Lys Leu Leu Gly Glu Glu Asn Lys Glu Asn Thr Pro Arg Asn 168 65 70 75 75 80 170 Val Leu Asn Ile Ile Pro Ala Ser Met Asn Tyr Ala Lys Ala His Ser 171 85 90 95 173 Lys Asp Lys Lys Lys Pro Gln Arg Asp Ser Gln Ala Gln Lys Ser Pro 174 \$100\$176 Val Lys Ser Lys Ser Thr His Arg Ile Gln His Asn Ile Asp Tyr Leu 177 $115 \qquad \qquad 120 \qquad \qquad 125$ 179 Lys His Leu Ser Lys Val Lys Lys Ile Pro Ser Asp Phe Glu Gly Ser 180 $$ 130 $$ 135 $$ 140 182 Gly Tyr Thr Asp Leu Gln Glu Arg Gly Asp Asn Asp Ile Ser Pro Phe 183 145 \$150\$185 Ser Gly Asp Gly Gln Pro Phe Lys Asp Ile Pro Gly Lys Gly Glu Ala 186 $$ 165 $$ 170 $$ 170 $$ 175 188 Thr Gly Pro Asp Leu Glu Gly Lys Asp Ile Gln Thr Gly Phe Ala Gly 189 180 185 190 191 Pro Ser Glu Ala Glu Ser Thr His Leu Asp Thr Lys Lys Pro Gly Tyr 192 195 200 205 194 Asn Glu Tie Pro Glu Arg Glu Glu Asn Gly Gly Asn Thr The Gly Thr 195 210 215 220197 Arg Asp Glu Thr Ala Lys Glu Ala Asp Ala Val Asp Val Ser Leu Val 198 225 ____ 230 ____ 235 ____ 240 200 Glu Gly Ser Asn Asp IIe Met Gly Ser Thr Asn Phe Lys Glu Leu Pro 201 245 250 255203 Gly Arg Glu Gly Asn Arg Val Asp Ala Gly Ser Gln Asn Ala His Gln 204 260265270 206 Gly Lys Val Glu Phe His Tyr Pro Pro Ala Pro Ser Lys Glu Lys Arg 207 275280285 280 209 Lys Glu Gly Ser Ser Asp Ala Ala Glu Ser Thr Asn Tyr Asn Glu Ile

 RAW SEQUENCE LISTING
 DATE: 01/23/2001

 PATENT APPLICATION:
 US/09/700,696
 TIME: 11:11:40

Input Set : A:\seq list.txt

Output Set: N:\CRF3\01232001\1700696.raw

```
210
        290
                             295
212 Pro Lys Asn Gly Lys Gly Ser Thr Arg Lys Gly Val Asp His Ser Asn
213 305
                       310
                                             315
215 Arg Asn Gln Ala Thr Leu Asn Glu Lys Gln Arg Phe Pro Ser Lys Gly
                    325
                                        330
                                                              335
218 Lys Ser Gln Cly Leu Pro 1le Pro Ser Arg Gly Leu Asp Asn Glu Tle
                                  345
                                                         350
219
               340
221 Lys Asn Glu Met Asp Ser Phe Asn Gly Pro Ser His Glu Asn Ile Ile
      355
                                360
                                                     365
224 Thr His Gly Arg Lys Tyr His Tyr Val Pro His Arg Cln Asn Asn Ser
     370
                           . 375
                                                 380
227 Thr Arg Asn Lys Gly Met Pro Gln Gly Lys Gly Ser Trp Gly Arg Gln
228 385
           390
                                            395
230 Pro His Ser Asn Arg Arg Phe Ser Ser Arg Arg Arg Asp Asp Ser Ser
         405
                            410
233 Glu Ser Ser Asp Ser Gly Ser Ser Ser Glu Ser Asp Gly Asp
234
               420
                                     425
238 <210> SEQ ID NO: 3
                                                            que source of genetic mateur
su circled port
de trem 12 on En
jun
239 <211> LENGTH: 4
240 <212> TYPE: PRT
241 <213> ORGANISM Artificial Sequence
244 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial
245 Sequence
247 <400> SEQUENCE: 3
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254 <211> LENGTH: 7
255 <212> TYPE: PRT
256 <213> ORGANISM Artificial Sequence
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259 <223> OTHER INTORMATION: Description of Artificial Sequence: Artificia Sequence: Artificia Sequence: Artificia Sequence 262 <400> SEQUENCE: 4
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264 1
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269 <211> LENGTH: 22
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271 <213> ORGÁNISM: Artificial Sequence
273 <220> FEATURE:
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277 <400> SEQUENCE: 5
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281 Ser Ser Glu Ser Asp Gly
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RAW SEQUENCE LISTING
                                                             DATE: 01/23/2001
                 PATENT APPLICATION: US/09/700,696
                                                            TIME: 11:11:40
                 Input Set : A:\seq list.txt
                 Output Set: N:\CRF3\01232001\I700696.raw
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287 <211> LENGTH: 21
288 <212> TYPE: PBF
289 <213> ORGANTSM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER LINEORMATION: Description of Artificial Sequence: Artificial Sequence: Artificial Sequence
295 <400> SEQUENCE: 6
296 Ser Ser Arg Ser Lys Glu Asp Ser Asn Ser Thr Glu Ser Lys Ser Ser
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299 Ser Glu Glu Asp Gly
300
                 20
304 <210> SEQ ID NO: 7
305 <211> LENGTH: 14
306 <212> TYPE: PRT
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial 311 Sequence 313 <400> SEQUENCE: 7
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315 1
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31.9 <21.0> SEQ ID NO: 8
320 <211> LENGTH: 38
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
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328 <400> SEQUENCE: 8
329 gacgacgaca aggtgaataa agaatatagt atcagtaa
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333 <211> LENGTH: 15
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335 <213> ORGANISM: Artificial Sequenc
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Description of Artificial Sequence Artificia 339 Sequence 341 <400> SEQUENCE: 9
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343 1
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349 <21.2> TYPE: PRT
                                                                        this event in subsequent sequerers
350 <213> ORGANISM Artificial Sequence
352 <220> FEATURE:
353 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificial Sequence:
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VERIFICATION SUMMARY

DATE: 01/23/2001 TIME: 11:11:41

PATENT APPLICATION: US/09/700,696

Input Set : A:\seq list.txt
Output Set: N:\CRF3\01232001\I700696.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date